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SEQUENCE LISTING

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<120> COMPOSITIONS AND METHODS FOR
TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES

<130> 8002-059

<150> 60/157,581
<151> 1999-10-04

<150> 60/157,637
<151> 1999-10-04

<160> 61

<170> FastSEQ for Windows Version 3.0

<210> 1
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<220>
<223> Forward primer

<400> 1
gaagatcttc cggaggaggg gaaatg 26

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<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 2
cgggatccga gctcgagggc ccgggaaagg atctaagaag atcc 44

<210> 3
<211> 477
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(474)

<400> 3
atg gta cgt agc tcc tct cgc act ccg tcc gat aag ccg gtt gct cat 48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
1 5 10 15

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gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt      96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
                20                  25                  30

cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctc cgt gat aac cag     144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
            35                  40                  45

ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg     192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
        50                  55                  60

ttc aag ggt cag ggc tgc ccg tcg act cat gtt ctg ctg act cac acc     240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
65                  70                  75                  80

atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc     288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
                85                  90                  95

gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg     336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
            100                 105                 110

aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag     384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
        115                 120                 125

aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat     432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
    130                 135                 140

ttc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg             474
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145                 150                 155

taa                                                                 477
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<210> 4
<211> 158
<212> PRT
<213> Homo sapiens

<400> 4

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Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 1               5                  10                  15
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
            20                  25                  30
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
        35                  40                  45
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
    50                  55                  60
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
65                  70                  75                  80
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
                85                  90                  95
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
            100                 105                 110
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
        115                 120                 125
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
    130                 135                 140
```

```
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145                 150                 155

      <210> 5
      <211> 28
      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Forward primer

      <400> 5
ccgacgcgtt gacacctgaa aactggag                                          28

      <210> 6
      <211> 29
      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Reverse primer

      <400> 6
ccgacgcgtg aaaggatctc aagaagatc                                         29

      <210> 7
      <211> 543
      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Fusion construct

      <221> CDS
      <222> (1)...(540)

      <400> 7
atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct  48
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1               5                  10                  15

acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc  96
Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
            20                  25                  30

gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag 144
Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
        35                  40                  45

ctg cag tgg ctg aac cgt cgc gct aac gcc ctg ctg gca aac ggc gtt 192
Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
    50                  55                  60

gag ctc cgt gat aac cag ctc gtg gta cct tct gaa ggt ctg tac ctg 240
Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
65                  70                  75                  80

atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tcg act cat 288
Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
                85                  90                  95
```

```
gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc      336
Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
            100                 105                 110

aaa gtt aac ctg ctg agc gct atc aag tct ccg tgc cag cgt gaa act      384
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
        115                 120                 125

ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt      432
Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
    130                 135                 140

ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac      480
Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
145                 150                 155                 160

cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt      528
Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
                165                 170                 175

att atc gca ctg taa                                                 543
Ile Ile Ala Leu
            180
```

<210> 8
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion construct

<400> 8

```
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1               5                  10                  15
Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
            20                  25                  30
Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
        35                  40                  45
Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
    50                  55                  60
Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
65                  70                  75                  80
Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
                85                  90                  95
Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
            100                 105                 110
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
        115                 120                 125
Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
    130                 135                 140
Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
145                 150                 155                 160
Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
                165                 170                 175
Ile Ile Ala Leu
            180
```

<210> 9
<211> 801
<212> DNA

<213> Artificial Sequence

<220>
<223> Fusion construct

<221> CDS
<222> (1)...(798)

<400> 9

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atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct        48
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1               5                  10                  15

acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac        96
Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
            20                  25                  30

aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt       144
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
        35                  40                  45

tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa       192
Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
    50                  55                  60

gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc       240
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
65                  70                  75                  80

tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att tct       288
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
                85                  90                  95

ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act       336
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
            100                 105                 110

ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat       384
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
        115                 120                 125

gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt       432
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
    130                 135                 140

ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc       480
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
145                 150                 155                 160

atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga       528
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
                165                 170                 175

ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc       576
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
            180                 185                 190

caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg       624
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
        195                 200                 205
```

```
aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc      672
Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
    210                 215                 220

tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac aga      720
Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
225                 230                 235                 240

att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat gaa      768
Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu
                245                 250                 255

gcc agt ttt ttc ggg gcc ttt tta gtt ggc taa                         801
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
            260                 265
```

<210> 10
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion construct

<400> 10

```
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1               5                  10                  15
Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
            20                  25                  30
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
        35                  40                  45
Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
    50                  55                  60
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
65                  70                  75                  80
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
                85                  90                  95
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
            100                 105                 110
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
        115                 120                 125
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
    130                 135                 140
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
145                 150                 155                 160
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
                165                 170                 175
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
            180                 185                 190
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
        195                 200                 205
Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
    210                 215                 220
Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
225                 230                 235                 240
Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu
                245                 250                 255
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
            260                 265
```

<210> 11
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construct

<221> CDS
<222> (1)...(462)

<400> 11

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atg aaa aag acg gct ctg gcg ctt ctg ctc ttg ctg tta gcg ctg act       48
Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr
 1               5                  10                  15

agt gta gcg cag gcc gct cct act agc tcg agc act aag aaa act caa       96
Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
            20                  25                  30

ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc      144
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
        35                  40                  45

atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa      192
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
    50                  55                  60

ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg      240
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65                  70                  75                  80

gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct      288
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95

aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta      336
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
            100                 105                 110

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac      384
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
        115                 120                 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc      432
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
    130                 135                 140

ttt gcc caa tcg atc att agc acg tta act taa                          465
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                 150
```

<210> 12
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion construct

<400> 12

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Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr
 1               5                  10                  15
Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
            20                  25                  30
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
        35                  40                  45
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
    50                  55                  60
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65                  70                  75                  80
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
            100                 105                 110
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
        115                 120                 125
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
    130                 135                 140
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                 150
```

<210> 13
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construct

<221> CDS
<222> (1)...(462)

<400> 13

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atg aaa cag tcg act ctg gcg ctt ctg ctc ttg ctg tta gcg ctg act      48
Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr
 1               5                  10                  15

agt gtg gcc aaa gcg gct cct act agc tcg agc act aag aaa act caa      96
Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
            20                  25                  30

ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc     144
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
        35                  40                  45

atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa     192
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
    50                  55                  60

ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg     240
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65                  70                  75                  80

gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct     288
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95

aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta     336
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
            100                 105                 110
```

```
atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac      384
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
        115                 120                 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc      432
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
    130                 135                 140

ttt gcc caa tcg atc att agc acg tta act taa                         465
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                 150
```

<210> 14
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion construct

<400> 14

```
Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr
 1               5                  10                  15
Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
            20                  25                  30
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
        35                  40                  45
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
    50                  55                  60
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65                  70                  75                  80
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
            100                 105                 110
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
        115                 120                 125
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
    130                 135                 140
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                 150
```

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 15
agtctagaca atcaggcgaa gaacgg 26

<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 16
agccatggag tcaccctcac ttttc 25

<210> 17
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 17
ggatccttaa gacccacttt cacatttaag t 31

<210> 18
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 18
ggttccatgg ttcacttttc tctatcac 28

<210> 19
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 19
gtgtccatgg ggcacagcca ccgcgacttc cag 33

<210> 20
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 20
acacgagctc ctacttggag gcagtcatga agct 34

<210> 21
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 21
gtgtccatgg ctcggcgggc aagtgtcggg actgaccatc atcatcatca tcatcacagc 60
caccgcgact tc 72

<210> 22
<211> 35
<212> DNA

<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 22
gtgcggatcc ctacttggag gcagtcatga agctg 35

<210> 23
<211> 16
<212> PRT
<213> Homo sapiens

<400> 23
Met Ala Arg Arg Ala Ser Val Gly Thr Asp His His His His His His
1 5 10 15

<210> 24
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence TiP 13.40

<400> 24
Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg
1 5 10 15
Val Val Met Tyr Glu Gly
20

<210> 25
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding TiP13.40

<400> 25
gcgtaccgct ggcgcctgtc ccatcgcccg aaaaccggct ttatccgcgt ggtgatgtac 60
gaaggc 66

<210> 26
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 26
gtgtactagt gtggcgcagg cggcgtaccg ctggcgcctg tcccatcgcc cgaaaaccgg 60
ctttatccgc gtggtgatgt acgaaggcta aggatccgcg c 101

<210> 27
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 27
gcgcggatcc ttagccttcg tacatcacca cgcggataaa gccggttttc gggcgatggg 60
acaggcgcca gcggtacgcc gcctgcgcca cactagtaca c 101

<210> 28
<211> 101
<212> PRT
<213> Homo sapiens

<400> 28
Met Ser Ser Ala Ala Gly Phe Cys Ala Ser Arg Pro Gly Leu Leu Phe
1 5 10 15
Leu Gly Leu Leu Leu Leu Pro Leu Val Val Ala Phe Ala Ser Ala Glu
20 25 30
Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr Ser
35 40 45
Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala Gly
50 55 60
Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly Arg
65 70 75 80
Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile Lys
85 90 95
Lys Leu Leu Glu Ser
100

<210> 29
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 29
cttcactagt gtggcgcagg cgaacggccg caaaatctgc ctggacctgc aggcgccgct 60
gtacaaaaaa atcatcaaaa aactgctgga aagctaagga tccgcg 106

<210> 30
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 30
cgcggatcct tagctttcca gcagtttttt gatgattttt ttgtacagcg gcgcctgcag 60
gtccaggcag attttgcggc cgttcgcctg cgccacacta gtgaag 106

<210> 31
<211> 85
<212> PRT
<213> Homo sapiens

<400> 31
Ile Tyr Ser Phe Asp Gly Arg Asp Ile Met Thr Asp Pro Ser Trp Pro
1 5 10 15
Gln Lys Val Ile Trp His Gly Ser Ser Pro His Gly Val Arg Leu Val
20 25 30
Asp Asn Tyr Cys Glu Ala Trp Arg Thr Ala Asp Thr Ala Val Thr Gly
35 40 45

Leu Ala Ser Pro Leu Ser Thr Gly Lys Ile Leu Asp Gln Lys Ala Tyr
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<220>
<223> Forward primer

<400> 35
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<210> 36
<211> 35
<212> DNA
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<220>
<223> Reverse primer

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<210> 37
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<400> 37
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<210> 41
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gacgcac 67

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<211> 71
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<213> Artificial Sequence

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<210> 44
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<213> Artificial Sequence

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<400> 44
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<400> 46
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<210> 47
<211> 33
<212> DNA
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<220>
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<400> 47
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<210> 48
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 48
cgcggatcct taggcactcg ccttgagtgc ctg 33

<210> 49
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 49
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gaagataccc cgccgggccc gtccaccgtg tttcgcccgc cg 102

<210> 50
<211> 103
<212> DNA
<213> Artificial Sequence

<220>
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<400> 50
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ccagcgggcg ggaggaggtc ggcgggcgaa acacggtgga cgg 103

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<211> 98
<212> DNA
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cgcatgaacg cgctgcagga agataccccg ccgggccc 98

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<212> DNA
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<220>
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<211> 551
<212> DNA
<213> Bacteriophage

<220>
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<222> (7)...(408)

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<222> (1)...(1)
<223> n=a, c, g, or t

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1 5 10

aac gcg ctg cag gaa gat acc ccg ccg ggc ccg tcc acc gtg ttt cgc 96
Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly Pro Ser Thr Val Phe Arg
15 20 25 30

ccg ccg acc tcc tcc cgc ccg ctg gaa acc ccg cat tgc cgc gaa atc 144
Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile
35 40 45

cgc atc ggc atc gcg ggc atc acc atc acc ctg tcc ctg tgc ggc tgc 192

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Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys
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gcg aac gcg cgc gcg ccg acc ctg cgc tcc gcg acc gcg gat aac tcc      240
Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser
        65                  70                  75

gaa aac acc ggc ttt aaa aac gtc ccg gat ctg cgc acc gat cag ccg      288
Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro
    80                  85                  90

aaa ccg ccg tcc aaa aaa cgc tcc tgc gat ccg tcc gaa tat cgc gtc      336
Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val
 95                 100                 105                 110

tcc gaa ctg aaa gaa tcc ctg atc acc acc acc ccg tcc cgc ccg cgc      384
Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro Ser Arg Pro Arg
                115                 120                 125

acc gcc cgc cgc tgc atc cgc ctc tgaaagcttg gctgttttgg cggatgagag     438
Thr Ala Arg Arg Cys Ile Arg Leu
            130

aagattttca gcctgataca gattaaatca gaacgcagaa gcggtctgat aaaacagaat    498
ttgcctggcg gcagtagcgc ggtggtccca cctgacccca tgccgaactc aga           551
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<210> 58
<211> 134
<212> PRT
<213> Bacteriophage

<400> 58

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            20                  25                  30
Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile Arg Ile
        35                  40                  45
Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys Ala Asn
    50                  55                  60
Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser Glu Asn
65                  70                  75                  80
Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro Lys Pro
                85                  90                  95
Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val Ser Glu
            100                 105                 110
Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro Ser Arg Pro Arg Thr Ala
        115                 120                 125
Arg Arg Cys Ile Arg Leu
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<210> 59
<211> 444
<212> DNA
<213> Bacteriophage

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<223> n=a, c, g, or t

<221> CDS

<222> (7)...(427)

<400> 59

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Arg Gln Arg Arg Arg Met Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly
 15                  20                  25                  30

ccg tcc acc gtg ttt cgc ccg ccg acc tcc tcc cgc ccg ctg gaa acc       144
Pro Ser Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr
                 35                  40                  45

ccg cat tgc cgc gaa atc cgc atc ggc atc gcg ggc atc acc atc acc       192
Pro His Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr
             50                  55                  60

ctg tcc ctg tgc ggc tgc gcg aac gcg cgc gcg ccg acc ctg cgc tcc       240
Leu Ser Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser
         65                  70                  75

gcg acc gcg gat aac tcc gaa aac acc ggc ttt aaa aac gtc ccg gat       288
Ala Thr Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp
     80                  85                  90

ctg cgc acc gat cag ccg aaa ccg ccg tcc aaa aaa cgc tcc tgc gat       336
Leu Arg Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp
 95                  100                 105                 110

ccg tcc gaa tat cgc gtc tcc gaa ctg aaa gaa tcc ctg atc acc acc       384
Pro Ser Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr
                115                 120                 125

acc ccg tcc cgc ccg cgc acc gcc cgc cgc tgc atc cgc ctc t             427
Thr Pro Ser Arg Pro Arg Thr Ala Arg Arg Cys Ile Arg Leu
            130                 135                 140

gaaagcttgg ctgtttt                                                   444
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<210> 60
<211> 140
<212> PRT
<213> Bacteriophage

<400> 60

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Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr Pro His
        35                  40                  45
Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser
    50                  55                  60
Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr
65                  70                  75                  80
Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg
                85                  90                  95
Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser
            100                 105                 110
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Ser Arg Pro Arg Thr Ala Arg Arg Cys Ile Arg Leu
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<212> DNA
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